

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/502,351
Source: PG/10
Date Processed by STIC: 3/3/05

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PCT

RAW SEQUENCE LISTING

DATE: 03/13/2005

PATENT APPLICATION: US/10/502,351

TIME: 12:06:41

Input Set : A:\2977-154 Sequence Listing.ST25.txt

Output Set: N:\CRF4\03132005\J502351.raw

3 <110> APPLICANT: Zhang, Lian Hui
 4 Lin, Yi Han
 5 Xu, Jin Liang
 7 <120> TITLE OF INVENTION: Ralstonia AHL-Acylase Gene
 9 <130> FILE REFERENCE: 2977-154
 11 <140> CURRENT APPLICATION NUMBER: 10/502351
 12 <141> CURRENT FILING DATE: 2004-07-23
 14 <150> PRIOR APPLICATION NUMBER: PCT/SG02/000011
 15 <151> PRIOR FILING DATE: 2002-01-23
 17 <160> NUMBER OF SEQ ID NOS: 7
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3743
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Ralstonia sp.
 27 <220> FEATURE:
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (16)..(16)
 30 <223> OTHER INFORMATION: n is a, c, g, or t
 32 <400> SEQUENCE: 1
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 35 cgcaccgaat ggcgcgcgcg gtgggcgcgc ggccgcgtggc cgggtgtggcg ccggatcagg 120
 37 cgccggaaagg cggacatgtc gtgataaccg cactgttcgg cgattgccgt caggctcagc 180
 39 gtgtctgactt ccagcagggtg gcaggcgccg tccacgcgcg cccgggtgcag caatgcagc 240
 41 ggccgagggtgc ccagggtctt ggtgaaatgc cgcagcagcg tgcgcgtcgct ggtcgaggcg 300
 43 gcccggccca gcttggccag gtcgaacgcg tcgtgcagggt gtcgtgcag gtacgcgcgc 360
 45 gcccgcgtta ccacgcgttgt gccggatggcg ggcttgcgtgc gcagccagat ggcgggtggac 420
 47 tcaccgcgcg acgggttggtc gaggcacggcc tggccgagggt tgccgtgcgc ccgggtgtcg 480
 49 gccaggcgcc cgaccaggcg ctgcgtgagc gcccacccgt gctccatcgc ggcgcgcgc 540
 51 agcacgttgc cgctgtgtac gatggcctgc tccgcacca cttcagctg cggtagttg 600
 53 ccgtgcagcc agccggcgat cagccacgtc accgtcaagc gccggccgcg gggcagcgcg 660
 55 ccggccagca ggcacgcgc ggtgaaggac gaggccacca acgcgtccgg cgtccaggta 720
 57 gcccggatg gtggcgctt cccactccag caggccagg cgctgtccca gctgtgtat 780
 59 gtggtcgaaa tgcaggggcg ggacgaccag cgcgtgcgcg agcgcggcggt cgcggcccg 840
 61 cagcggctgg cagcggcagg ccagggtctc ggccggccgc tgccagcggg ccgggtcgcg 900
 63 cgcgaccagc cgcacccga acacggggct ggccgcgtcg gcacgcgttc cggcatgc 960
 65 ggaggcgagc gcattggcca cgcgcagggt gtcggcgacg gtcgcgcgcg tggagaggcc 1020
 67 ggcgtcgaga aagggtcagca ggtcgatgtc ggcacccgcg aagtataggg gagggcgccg 1080
 69 gaggccttcgt gctgtggcggt attgacccca actctggcggt gaataacctt ttccctccggg 1140
 71 cggccccag tcgacgatac ggcgggtggct ggcgcgtgc gccgcgcgaa gactagagcg 1200
 73 acacaagaca agaccgacaa caggagacaa cgcacgtatgc agggattcgc gctgcgcggc 1260
 75 acgtctgcgcg tggccgcgtc cgcggcgctg gccggctgcg ccagttccac cgtggccgc 1320
 77 tgggggtcgcc tcagcgacac cggcctgtcc gccgagatcc gccgcaccgg cttcggcatt 1380

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79	ccgcacatcc	gcccAACG	ctacGCCAGC	ctcgGCTATG	gcatGGCCTA	tgcCTACGCG	1440									
81	caggacaacc	tgtGCCTGCT	ggccGACCAG	gtggTCACCG	tcaACGGCGA	gCGCTCGAAG	1500									
83	acttcgggc	ccgAGGGCAC	cgtGACGGTC	tcgttCAAGC	cgatCCCCAA	cctGCAAGTCG	1560									
85	gacgcTTCT	tcaAGGGCAT	cttcGACGAG	gacGGCCTGC	gCGCCGGTTA	tgcGAGATG	1620									
87	tcgcccGAGG	cgcGCGAGCT	gctGCGCGC	tacATCGCCG	gCTTCAACCG	ctatCTCAAG	1680									
89	gacaCGCCG	ccgCCAACTT	cccGGCCGC	tgCCGCAATG	ccgCCGGGT	gCGTCCGCTC	1740									
91	acgttGGCG	acatGATGCG	catGGGCGAA	gagaAGGCGA	tccAGGCCAG	cgCCGGCGCC	1800									
93	atgttGGCGG	gcatGTCG	cgcGCAgCCG	ccggGGCGCA	cgCCGGTGGC	cgAGCGCGAG	1860									
95	attccGCCG	aggCCGTCGA	caccGTGGCG	ctggACCGCG	aactGCAgCT	gCGCACATG	1920									
97	ccgatCGGCT	ccaACGGCTG	ggcCTTCGGC	gctGACGCCA	ccgCCAACCG	gCGCGGCGTG	1980									
99	ctgtCTCGGCA	atccGCACTT	ccCGTGGACG	accACCAACC	gCTTCTACCA	ggtCCACCTG	2040									
101	acggTGCCTG	gcaAGCTCGA	cgtGATGGC	gcCTCGATCG	cgGCCTTCCC	ggtGGTgAGC	2100									
103	atcgGCTTCA	acaAGGACGT	ggcGTGGACG	cacACCCTCT	ccaccGGGCG	ccGCTTCACC	2160									
105	ttgttCGAAC	tgaAGCTGGC	cgaAGGCGAC	ccgACCACCT	acctGGTCGA	cgGCACGCCG	2220									
107	cacaAGATGA	ccACCCGCAc	ggtGCGCTTC	gacGTCAGC	tgCCGGACGG	ccGCTCGAG	2280									
109	cgCCGCAcG	acacCTTCTA	cgACACCCATC	tacGGCCCGG	tgCTGTGAT	gCCGAGCGGC	2340									
111	ggcatGCCGT	ggACCACGCA	gaAGGCCTAC	gccCTGCGCG	acGCCAACCG	caACAACACG	2400									
113	cgCTCGGTG	acAGCTGGCT	gcatATCGGG	caggCCCGGG	acGtGGCCGG	catCCGCCAG	2460									
115	gccatCGGCA	acCTGGGCA	tccCTGGGT	aaCACCATCG	ccaccGACCG	caACGGCCG	2520									
117	gCGCTGTTG	ccgACGTGTC	gaccACGCCG	gacGtGCCGG	ccGCGGAGCT	ccAGCGCTGT	2580									
119	gccccGTCG	cgCTGGCCGG	caaACTCTC	aaggACGCCG	gcCTGGTGT	gCTGACGGC	2640									
121	tcgeGCGGCA	cctGCAACTG	gGAGGTCGAT	ccGGCTTCG	cggtACCCGG	gctGGTGGCG	2700									
123	ccCGCGCGCA	tgCCGGTGT	cgAGCGCGAC	gactACGTG	ccaACAGCAA	tgACAGCTCC	2760									
125	tggCTGACCA	acCCCGCGCA	aaAGCTGACC	ggCTTCTCGC	cggtGATGGG	ctCGGTGAC	2820									
127	gtACCGCAGC	ggCTGCGCAC	gGcACATCGGC	ctGATCGAGA	tcggCCGCCG	cctGGCCGGC	2880									
129	accGACGGAC	tgCCCGGCAA	ccGCAcTCGAT	ctGCGAACC	tgCAGGCGAT	gatCTTCAGC	2940									
131	aatGCCAACC	tggCGGGACA	actGGTGTG	ggcGACCTGC	tcgCGGCGATG	caAGGCCACG	3000									
133	ccggCCCCGG	atGCCGACGT	gGCGCACGCG	tgCCGCCGCC	tcggCCAGTG	gaACCGCACC	3060									
135	agcaACGCCG	acGCCCCGCG	cgcGcacCTG	ttCCGCGAGT	tctGGATGCG	cgCCAAGGAC	3120									
137	atCGCGCAGG	tgcACGCCGT	cgAGTTGCGAC	ccggCCGACC	cggtCCACAC	gCCGCGCGGC	3180									
139	ctGCGCATGA	acGACGCGAC	ggtACGCAcG	gCGGTGTTCA	aggCGCTGAA	ggaAGCCGTG	3240									
141	ggCGCGGTG	gcaAGGCGGG	cttCGCGCTG	gatGCGCCGC	tggGCACGGT	acAGGCCGCG	3300									
143	cacGCAACCGG	acGGCTCCAT	cgCCCTGCAc	ggCGGCCGAGG	aatacGAAGG	cgtGCTCAAC	3360									
145	aagCTGCAA	ccCTGCCGAT	cgGGGCCGAAG	ggGCTGCCGG	tgtATTTCGG	caccAGCTAC	3420									
147	atCCAGACCG	tgACCTTCGA	cgACCAAGGGC	ccGGTGCCTG	acGCCATCCT	cacctACGGC	3480									
149	gaatCGACCG	accACGCCCTC	gCCGACCGCG	ttcGACCGAGA	tgcGtGCGTA	ctCGGGCAAG	3540									
151	cactGGAACC	ggCTGCCGTT	ctCCGAAAGCG	gccATCGEGG	ccGATCCGGC	gCTGAAGGTG	3600									
153	atGCGGTTGT	cgcAGTGTGAGG	gctGCCGGTG	cctGAAaaa	cgCCCCGCTT	gtGCGGGGGCG	3660									
155	ttttttGCG	agtGTGAATG	gctCAATG	gttGAAACC	gcatCCGGAC	atGACTGTAT	3720									
157	tgtGACTCTG	cctGtGTCGG	tGT				3743									
160	<210>	SEQ ID NO:	2													
161	<211>	LENGTH:	794													
162	<212>	TYPE:	PRT													
163	<213>	ORGANISM:	Ralstonia sp.													
165	<400>	SEQUENCE:	2													
167	Met	Met	Gln	Phe	Ala	Leu	Arg	Gly	Thr	Leu	Ala	Met	Ala	Ala	Leu	
168	1				5				10				15			
171	Ala	Ala	Leu	Ala	Gly	Cys	Ala	Ser	Ser	Thr	Asp	Gly	Arg	Trp	Gly	Ser
172						20				25			30			

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175 Leu Ser Asp Thr Gly Leu Ser Ala Glu Ile Arg Arg Thr Gly Phe Gly
176 35 40 45
179 Ile Pro His Ile Arg Ala Asn Asp Tyr Ala Ser Leu Gly Tyr Gly Met
180 50 55 60
183 Ala Tyr Ala Tyr Ala Gln Asp Asn Leu Cys Leu Leu Ala Asp Gln Val
184 65 70 75 80
187 Val Thr Val Asn Gly Glu Arg Ser Lys Thr Phe Gly Pro Glu Gly Thr
188 85 90 95
191 Val Thr Val Ser Phe Lys Pro Ile Pro Asn Leu Gln Ser Asp Ala Phe
192 100 105 110
195 Phe Lys Gly Ile Phe Asp Glu Asp Gly Leu Arg Ala Gly Tyr Ala Gln
196 115 120 125
199 Met Ser Pro Glu Ala Arg Glu Leu Leu Arg Gly Tyr Ile Ala Gly Phe
200 130 135 140
203 Asn Arg Tyr Leu Lys Asp Thr Pro Pro Ala Asn Phe Pro Ala Ala Cys
204 145 150 155 160
207 Arg Asn Ala Ala Trp Val Arg Pro Leu Thr Leu Gly Asp Met Met Arg
208 165 170 175
211 Met Gly Glu Glu Lys Ala Ile Gln Ala Ser Ala Gly Ala Met Leu Ala
212 180 185 190
215 Gly Ile Val Ala Ala Gln Pro Pro Gly Arg Thr Pro Val Ala Glu Arg
216 195 200 205
219 Glu Ile Pro Pro Gln Ala Val Asp Thr Val Ala Leu Asp Arg Glu Leu
220 210 215 220
223 Gln Leu Arg Asp Met Pro Ile Gly Ser Asn Gly Trp Ala Phe Gly Ala
224 225 230 235 240
227 Asp Ala Thr Ala Asn Arg Arg Gly Val Leu Leu Gly Asn Pro His Phe
228 245 250 255
231 Pro Trp Thr Thr Asn Arg Phe Tyr Gln Val His Leu Thr Val Pro
232 260 265 270
235 Gly Lys Leu Asp Val Met Gly Ala Ser Ile Ala Ala Phe Pro Val Val
236 275 280 285
239 Ser Ile Gly Phe Asn Lys Asp Val Ala Trp Thr His Thr Val Ser Thr
240 290 295 300
243 Gly Arg Arg Phe Thr Leu Phe Glu Leu Lys Leu Ala Glu Gly Asp Pro
244 305 310 315 320
247 Thr Thr Tyr Leu Val Asp Gly Thr Pro His Lys Met Thr Thr Arg Thr
248 325 330 335
251 Val Ala Phe Asp Val Lys Leu Pro Asp Gly Arg Leu Glu Arg Arg Thr
252 340 345 350
255 His Thr Phe Tyr Asp Thr Ile Tyr Gly Pro Val Leu Ser Met Pro Ser
256 355 360 365
259 Gly Gly Met Pro Trp Thr Thr Gln Lys Ala Tyr Ala Leu Arg Asp Ala
260 370 375 380
263 Asn Arg Asn Asn Thr Arg Ser Val Asp Ser Trp Leu His Ile Gly Gln
264 385 390 395 400
267 Ala Arg Asp Val Ala Gly Ile Arg Gln Ala Ile Gly Asn Leu Gly Ile
268 405 410 415
271 Pro Trp Val Asn Thr Ile Ala Thr Asp Arg Asn Gly Arg Ala Leu Phe

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272	420	425	430	
275	Ala Asp Val Ser Thr Thr Pro Asp Val Pro Ala Ala Glu Leu Gln Arg			
276	435	440	445	
279	Cys Ala Pro Ser Pro Leu Ala Gly Lys Leu Phe Lys Asp Ala Gly Leu			
280	450	455	460	
283	Val Leu Leu Asp Gly Ser Arg Gly Thr Cys Asn Trp Gln Val Asp Pro			
284	465	470	475	480
287	Ala Ser Pro Val Pro Gly Leu Val Ala Pro Ala Arg Met Pro Val Leu			
288	485	490	495	
291	Glu Arg Asp Asp Tyr Val Ala Asn Ser Asn Asp Ser Ser Trp Leu Thr			
292	500	505	510	
295	Asn Pro Ala Gln Lys Leu Thr Gly Phe Ser Pro Val Met Gly Ser Val			
296	515	520	525	
299	Asp Val Pro Gln Arg Leu Arg Thr Arg Ile Gly Leu Ile Glu Ile Gly			
300	530	535	540	
303	Arg Arg Leu Ala Gly Thr Asp Gly Leu Pro Gly Asn Arg Ile Asp Leu			
304	545	550	555	560
307	Pro Asn Leu Gln Ala Met Ile Phe Ser Asn Ala Asn Leu Ala Gly Gln			
308	565	570	575	
311	Leu Val Leu Gly Asp Leu Leu Ala Ala Cys Lys Ala Thr Pro Ala Pro			
312	580	585	590	
315	Asp Ala Asp Val Arg Asp Gly Cys Ala Ala Leu Gly Gln Trp Asn Arg			
316	595	600	605	
319	Thr Ser Asn Ala Asp Ala Arg Ala Ala His Leu Phe Arg Glu Phe Trp			
320	610	615	620	
323	Met Arg Ala Lys Asp Ile Ala Gln Val His Ala Val Glu Phe Asp Pro			
324	625	630	635	640
327	Ala Asp Pro Val His Thr Pro Arg Gly Leu Arg Met Asn Asp Ala Thr			
328	645	650	655	
331	Val Arg Thr Ala Val Phe Lys Ala Leu Lys Glu Ala Val Gly Ala Val			
332	660	665	670	
335	Arg Lys Ala Gly Phe Ala Leu Asp Ala Pro Leu Gly Thr Val Gln Ala			
336	675	680	685	
339	Ala His Ala Pro Asp Gly Ser Ile Ala Leu His Gly Gly Glu Glu Tyr			
340	690	695	700	
343	Glu Gly Val Leu Asn Lys Leu Gln Thr Leu Pro Ile Gly Pro Lys Gly			
344	705	710	715	720
347	Leu Pro Val Tyr Phe Gly Thr Ser Tyr Ile Gln Thr Val Thr Phe Asp			
348	725	730	735	
351	Asp Gln Gly Pro Val Ala Asp Ala Ile Leu Thr Tyr Gly Glu Ser Thr			
352	740	745	750	
355	Asp His Ala Ser Pro His Ala Phe Asp Gln Met Arg Ala Tyr Ser Gly			
356	755	760	765	
359	Lys His Trp Asn Arg Leu Pro Phe Ser Glu Ala Ala Ile Ala Ala Asp			
360	770	775	780	
363	Pro Ala Leu Lys Val Met Arg Leu Ser Gln			
364	785	790		
367	<210> SEQ ID NO: 3			
368	<211> LENGTH: 785			

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369 <212> TYPE: PRT
 370 <213> ORGANISM: Deinococcus radiodurans
 372 <400> SEQUENCE: 3
 374 Met Ser Arg Ser Pro Phe Ser Ser Val Ser Leu Pro Ala Arg Leu Leu
 375 1 5 10 15
 378 Leu Gly Ser Leu Leu Leu Gly Pro Leu Met Leu Gly Gly Ala Ala Ser
 379 20 25 30
 382 Ala Gln Thr Tyr Gln Val Gln Ile Gln Arg Thr Ala His Gly Ile Pro
 383 35 40 45
 386 His Ile Gln Ala Ser Asp Leu Gly Gly Ile Gly Tyr Gly Val Gly Tyr
 387 50 55 60
 390 Ser Tyr Ala Gln Asp Asn Leu Cys Leu Leu Ala Asp Gln Val Met Thr
 391 65 70 75 80
 394 Val Arg Gly Glu Arg Ser Lys Phe Leu Gly Ala Glu Gly Lys Thr Val
 395 85 90 95
 398 Val Gly Phe Gln Pro Val Asn Asn Leu Asp Ser Asp Val Phe Phe Lys
 399 100 105 110
 402 Thr Val Ile Glu Pro Gly Arg Leu Gln Ala Gly Tyr Arg Asp Gln Pro
 403 115 120 125
 406 Gln Ile Leu Ala Leu Met Arg Gly Tyr Val Ala Gly Val Asn Arg Tyr
 407 130 135 140
 410 Leu Arg Asp Thr Pro Pro Glu Gln Trp Pro Ser Ala Cys Arg Asn Ala
 411 145 150 155 160
 414 Asp Trp Val Arg Pro Leu Thr Glu Leu Asp Val Met Arg Leu Gly Glu
 415 165 170 175
 418 Glu Lys Ala Ile Gln Ala Ser Ala Gly Ala Met Val Ser Ala Ile Thr
 419 180 185 190
 422 Ser Ala Arg Pro Pro Gln Ala Gly Ala Ser Thr Ala Ala Pro Arg Pro
 423 195 200 205
 426 Asp Leu Ala Ala Phe Asn Arg Gln Tyr Arg Phe Asn Asp Leu Pro Ile
 427 210 215 220
 430 Gly Ser Asn Gly Trp Ala Phe Gly Ser Glu Ala Thr Thr Asn Gly Arg
 431 225 230 235 240
 434 Gly Leu Leu Leu Gly Asn Pro His Phe Pro Trp Glu Thr Ser Asn Arg
 435 245 250 255
 438 Phe Tyr Gln Leu His Leu Thr Leu Pro Gly Gln Phe Asp Val Met Gly
 439 260 265 270
 442 Ala Ser Leu Gly Gly Met Pro Val Val Asn Ile Gly Phe Asn Gln Asp
 443 275 280 285
 446 Val Ala Trp Thr His Thr Val Ser Thr Asp Lys Arg Phe Thr Leu Ala
 447 290 295 300
 450 Ala Leu Thr Leu Val Pro Gly Asp Pro Leu Ser Tyr Val Lys Asp Gly
 451 305 310 315 320
 454 Gln Gln Arg Arg Leu Gln Arg Arg Thr Ala Val Ile Glu Val Lys Thr
 455 325 330 335
 458 Ala Asn Gly Pro Arg Leu His Thr Arg Thr Val Tyr Phe Thr Pro Glu
 459 340 345 350
 462 Gly Pro Leu Val Asn Leu Pro Ala Ala Gly Leu Thr Trp Thr Pro Gln
 463 355 360 365

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/13/2005
PATENT APPLICATION: US/10/502,351 TIME: 12:06:42

Input Set : A:\2977-154 Sequence Listing.ST25.txt
Output Set: N:\CRF4\03132005\J502351.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 16

VERIFICATION SUMMARY

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L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:999 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7

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